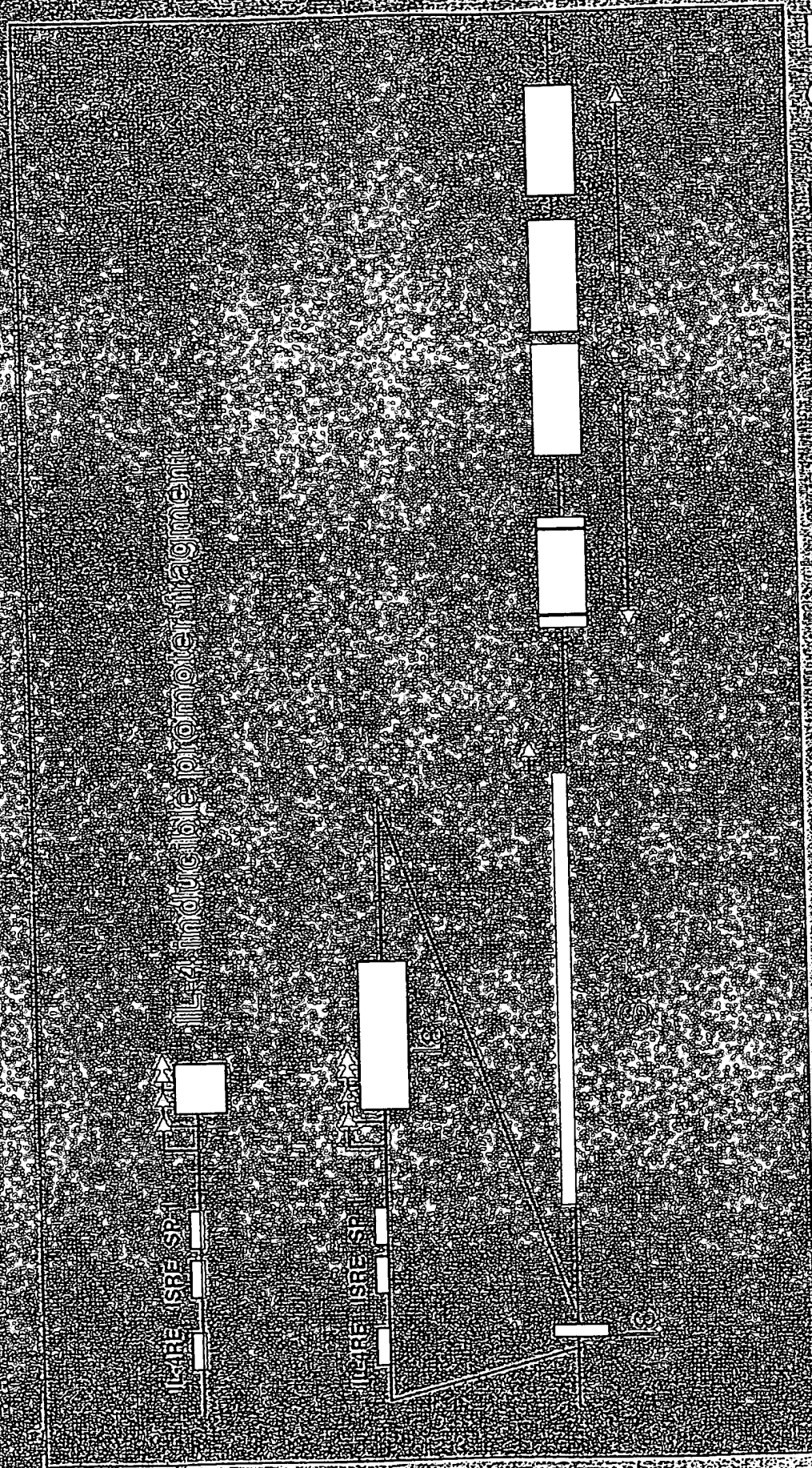


FIGURE 1A

CTCGAGGACAGTGACCTGGGAGTGAGTACAAGGTGAGGCCACCACTCAGGGT
GCCAGCTCCAAGCGGGTCACAGGGACGAGGGCTGCGGCCATCAGGAGGCCCT
GCACACACATCTGGGACACGCGCCCCCGAGGGCCAGTTCACCTCAGTGCGCCT
CATTCTCCTGCACAAAAGCGCCCCCATCCTTTCTTCACAAGGCTTTCGTGGAAG
CAGAGGCGTCGATGCCCAGTACCCTCTCCCTTTCCCAGGCAACGGGACCCCAA
GTTTGCTGACTGGGACCACCAAGCCACGCATGCGTCAAGAGTGAGAGTCCGG
GACCTAGGCAGGGGGCCCTGGGGTTGGGCCTGAGAGAGAAGAGAACCTCCCCC
AGCACTCGGTGTGCATCGGTAGTGAAGGAGCCTCACCTGACCCCGCTGTTGC
TCAATCGACTTCCCAAGAACAGAGAGAAAAGGGAACCTCCAGGGCGGCCCCG
GCCTCCTGGGGGTTCCCACCCCATTTTTAGCTGAAAGCACTGAGGCAGAGCTC
CCCCTACCCAGGCTCCACTGCCCCGGCACAGAAATAACAACCACGGTTACTGAT
CATCTGGGAGCTGTCCAGGAATTC

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Germ-line Locus



TRIGEL

FIGURE 1B

Low energy DNA folding of the S_{ϵ} region

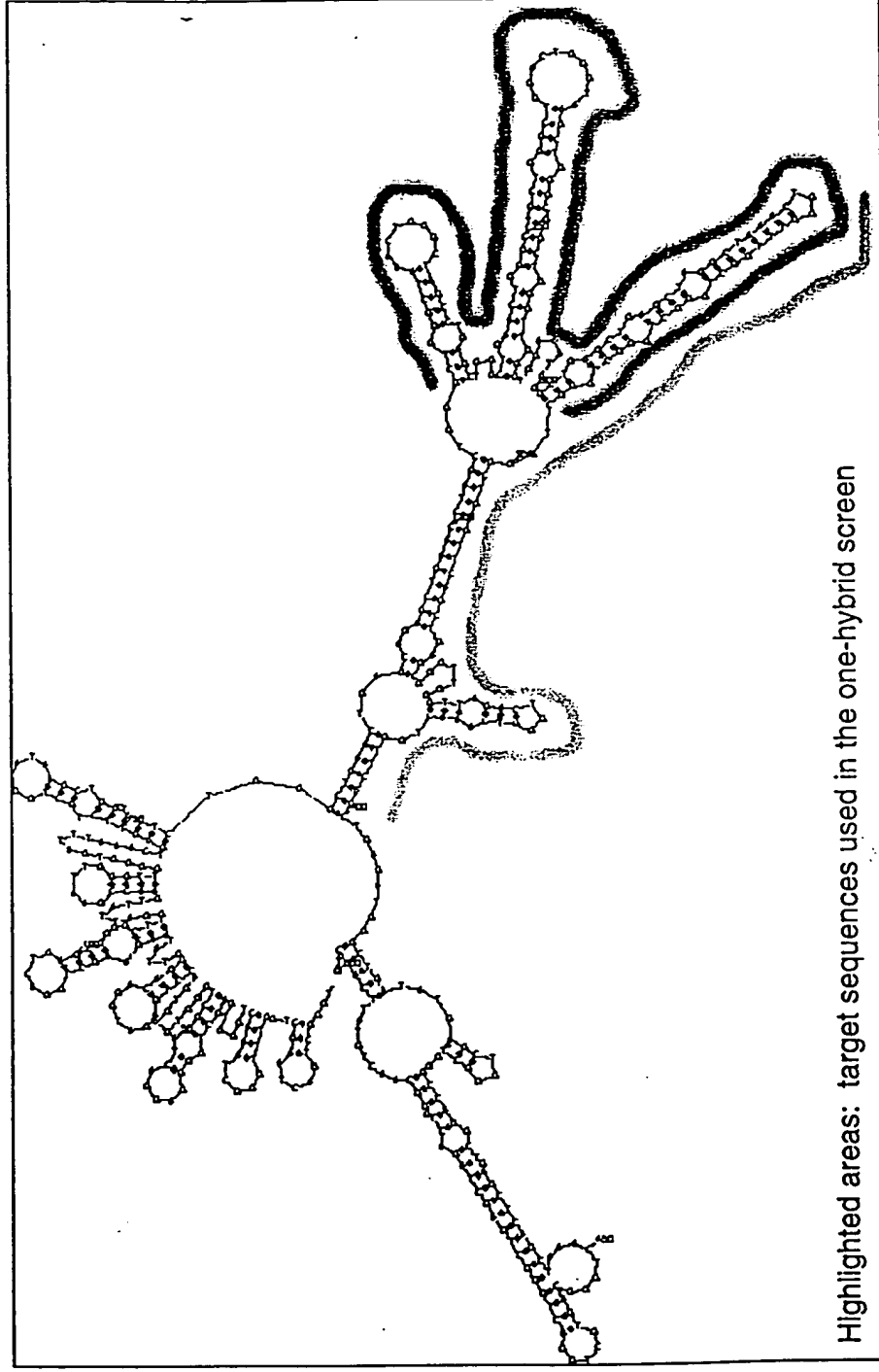


FIG 2A

FIGURE 2B

1 GCTGGGCTAA ACTGGGCTAG CCTGAGCTGG GCTGAACTGG GCTGCTGGGC
51 TGGACTGGGT AAGCTGGGCT GAGCTGGGTT GGGTGGAAAT GGGCTGAGCT
101 GAGCTAGGCT AACTGGGTT TGGCTGGGCT GGGCTGGGCT GGG

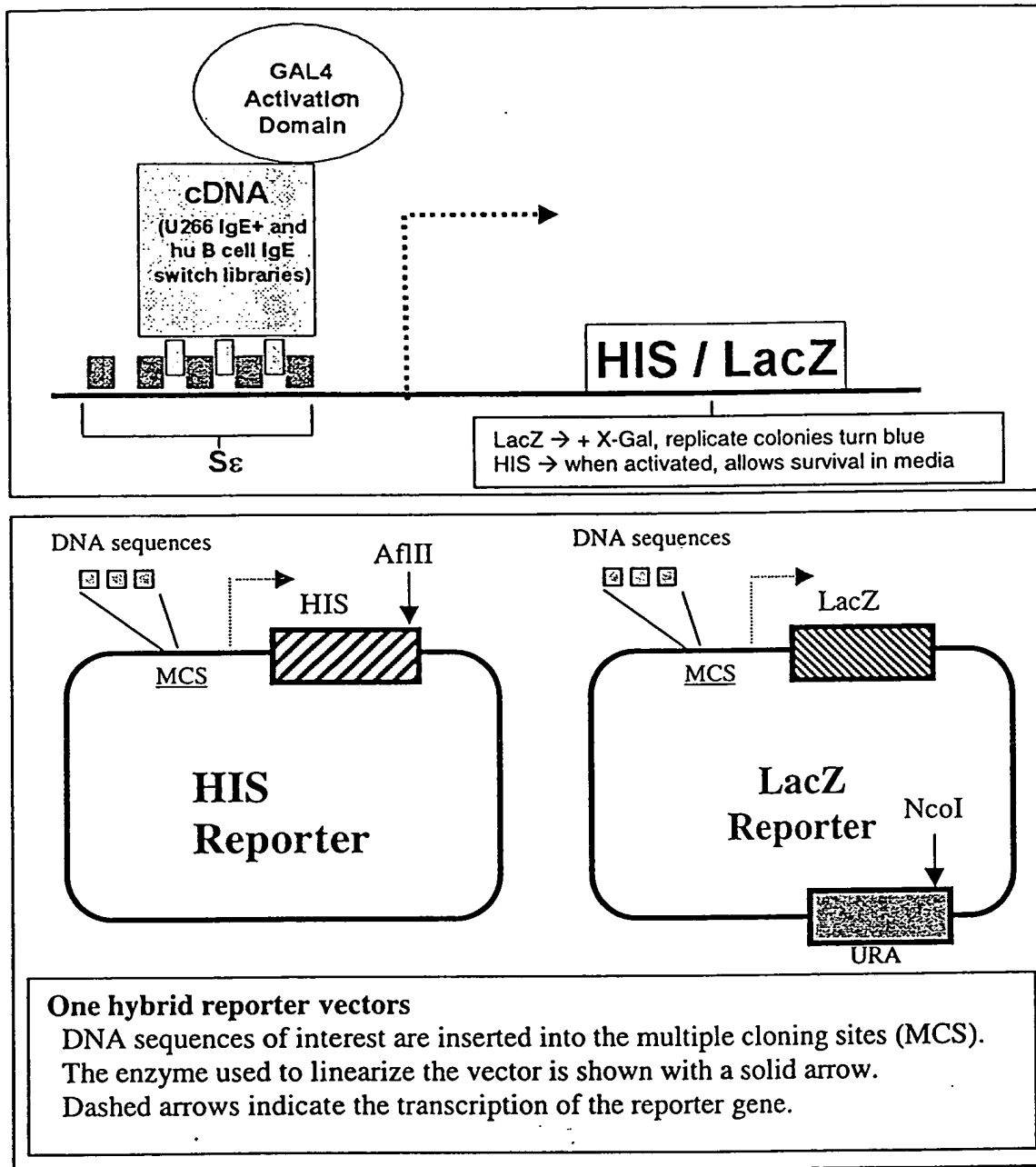
FIGURE 2C

1 GGTTTGGCTG GGCTGGGCTG GGCTGGGCTG GGTTTCAGCTG AGCGGGTTGG
51 GTTAGACTGG GTCAAACCTGG TTCAGC

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FIG 3

Appendix F Yeast One-Hybrid Screening



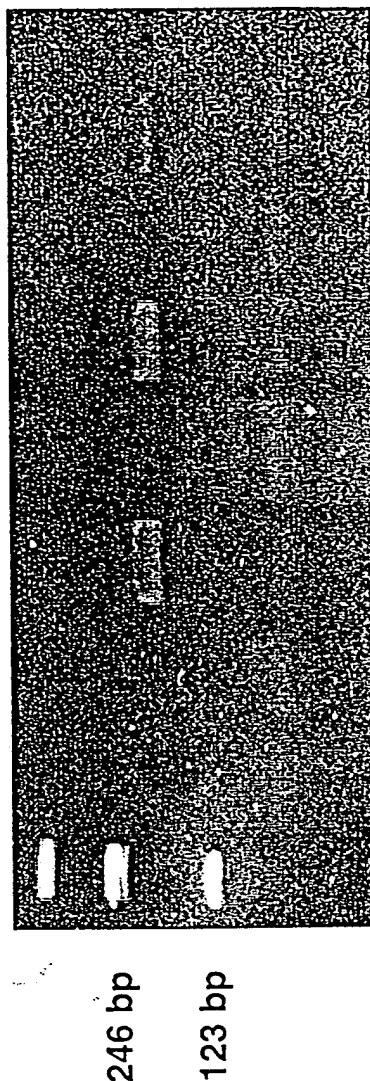
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FIG 4

IL-4 Induction of Germline ϵ mRNA in the IgM+ B cell lines: CA-46, MC-116 and DND39

Cells were incubated for 48 hrs in 300 U/ml of h-IL-4. RT-PCR was performed using primers specific for the germline ϵ exon and the 5'-end of the ϵ CH1 exon (predicted size ~ 200 bp).

DND39 + IL-4
DND39 - IL-4
MC-116 + IL-4
MC-116 - IL-4
CA-46 + IL-4
CA-46 - IL-4
Neg cont.



Approaches to generate germine ϵ promoter knock-in reporter cell lines

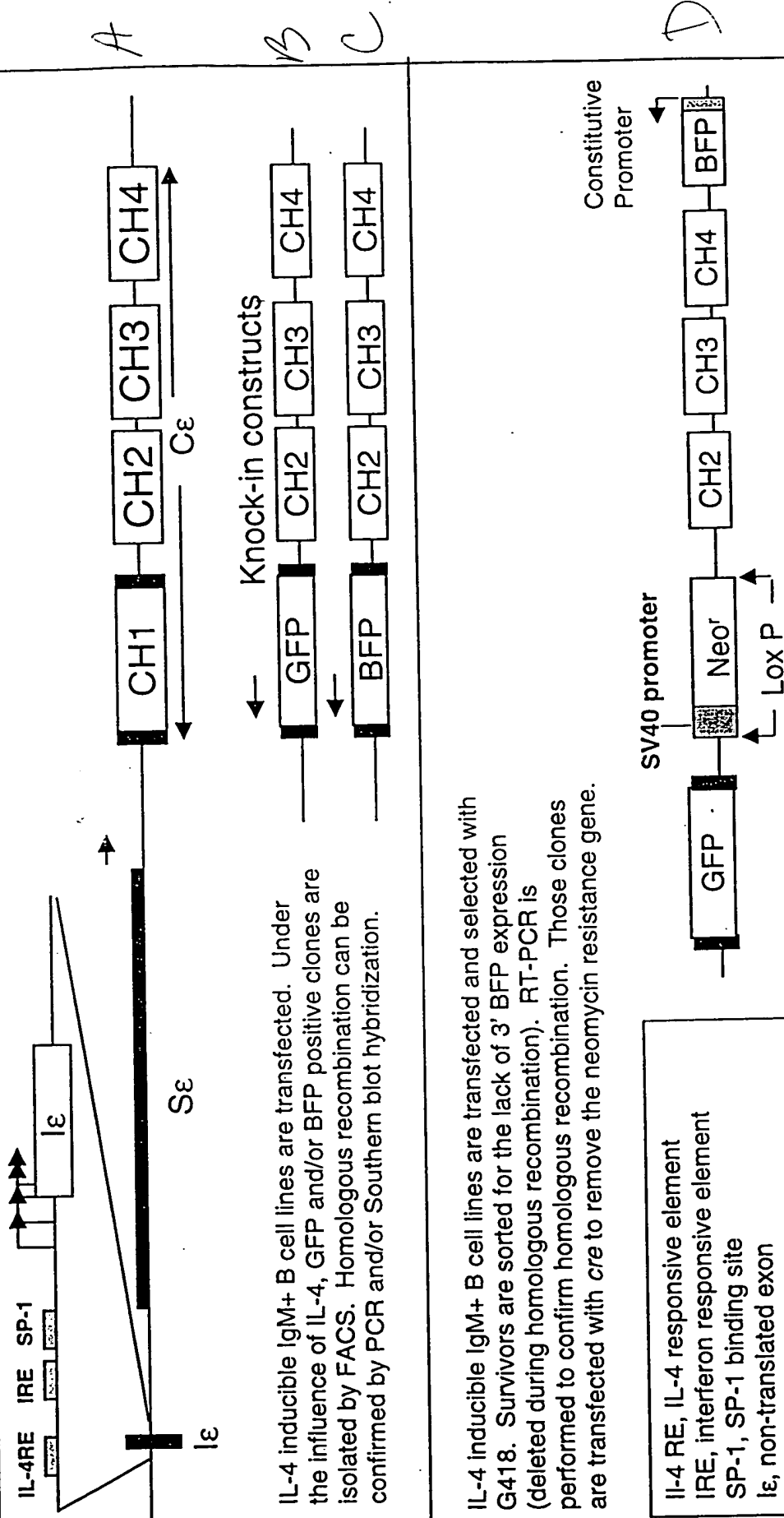
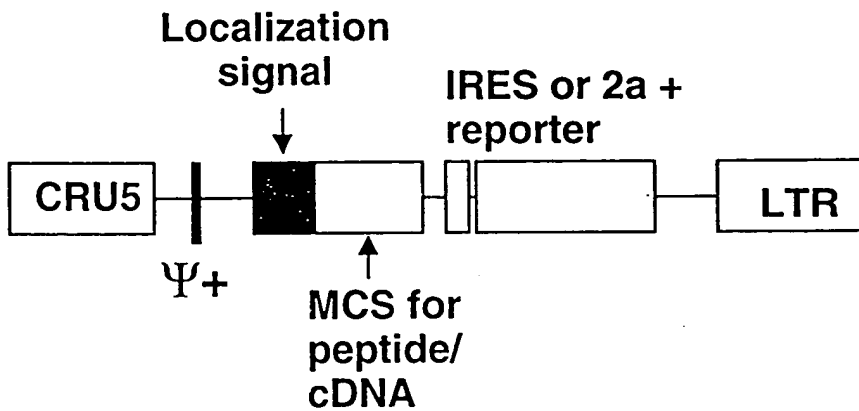


FIG 6

Appendix I

Rigel Base Vector



All components are cassetted for flexibility

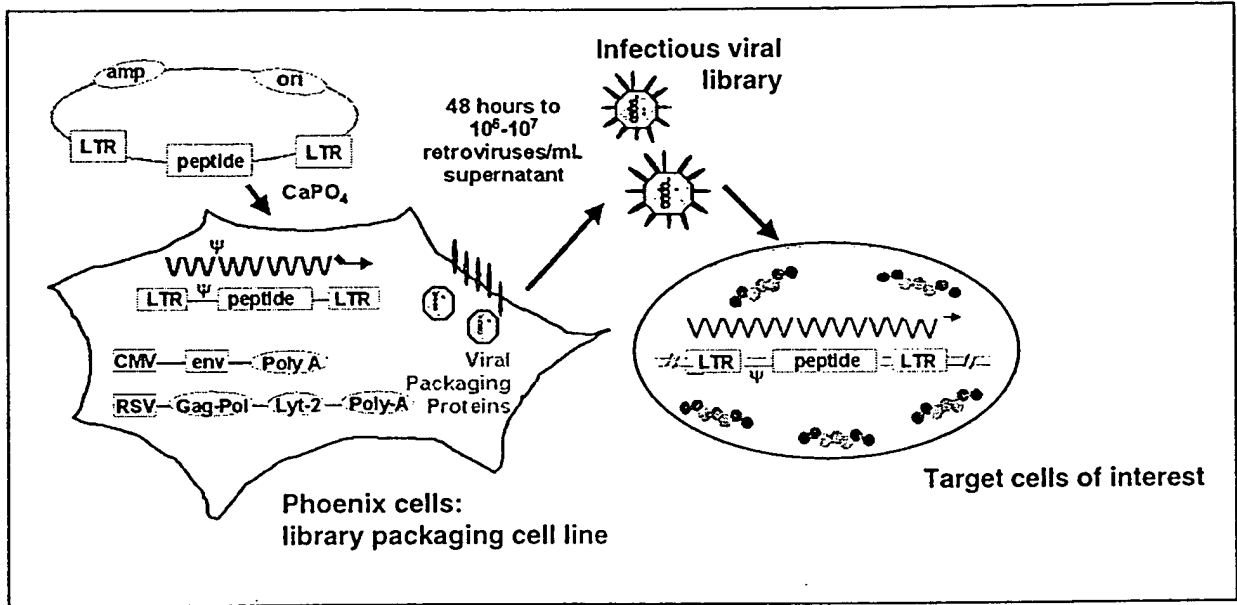
CRU5, modified LTR
LTR, long terminal repeat
Ψ+, packaging signal
Localization signal: nuclear, cell membrane, granular
MCS, multiple cloning site
IRES, internal ribosome entry site
2a, self-cleaving peptide

092504 092504 092504

FIG 7

Appendix H

Protocol for Transfection of Phoenix Cells and Infection of Nonadherent Target Cells

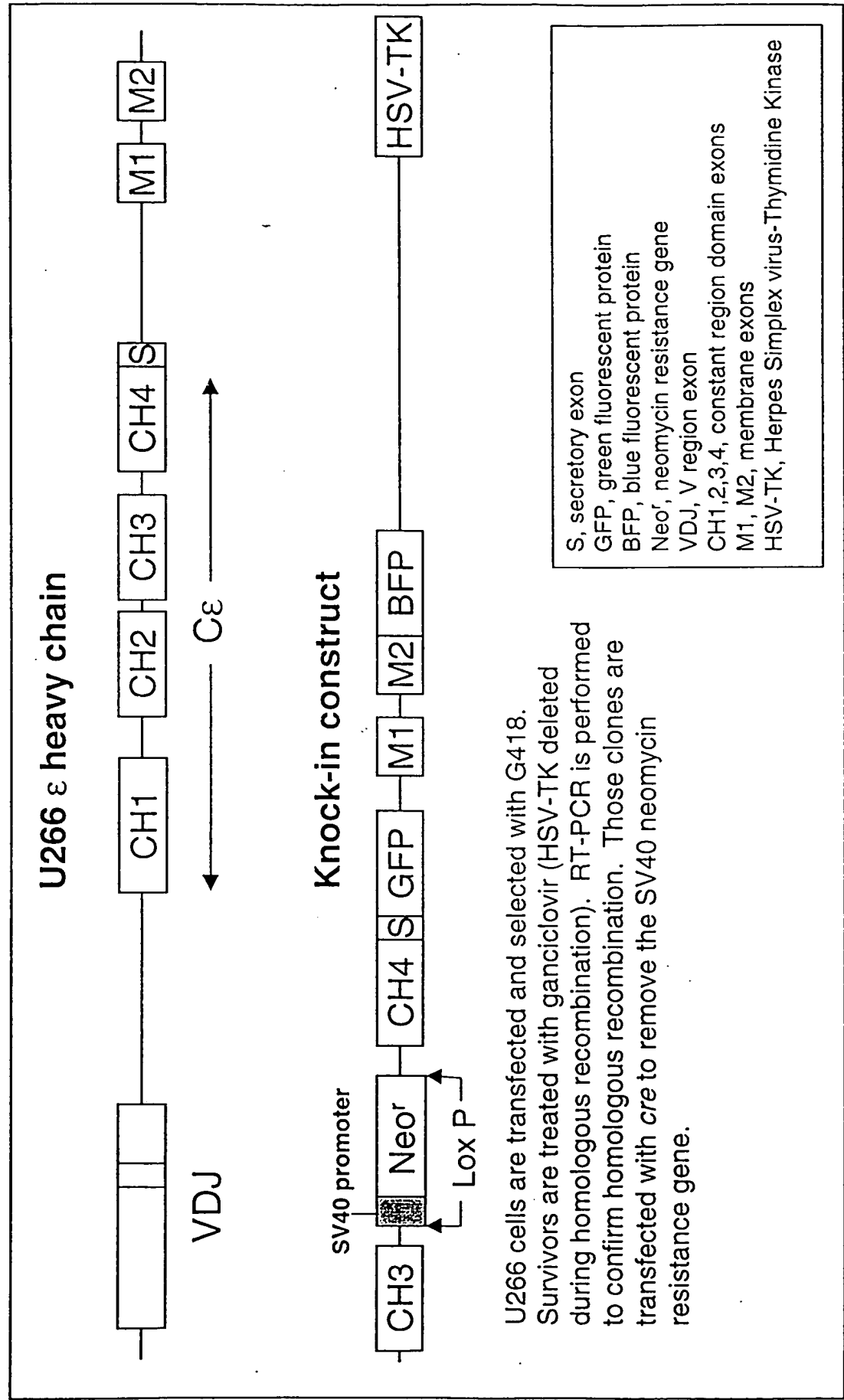


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FIG 8

205250-42E9660

ϵ heavy chain GFP/BFP knock-in cell line

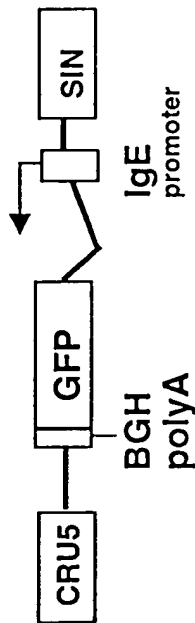


U266 cells are transfected and selected with G418. Survivors are treated with ganciclovir (HSV-TK deleted during homologous recombination). RT-PCR is performed to confirm homologous recombination. Those clones are transfected with *cre* to remove the SV40 neomycin resistance gene.

Appendix D

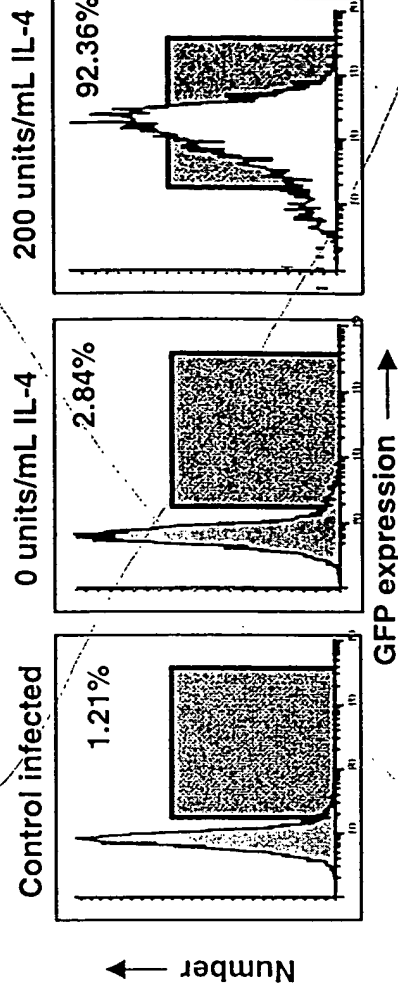
IL-4 Inducible ϵ Promoter Reporter Cell Line

Reporter construct



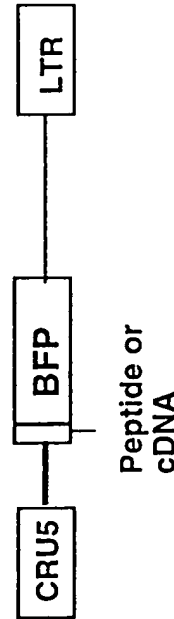
CRU5, hCMV promoter plus R and U5 regions of LTR
 GFP, green fluorescent protein
 BGH poly A, bovine growth hormone poly-adenylation signal
 SIN, self-inactivating LTR

IL-4 induced reporter



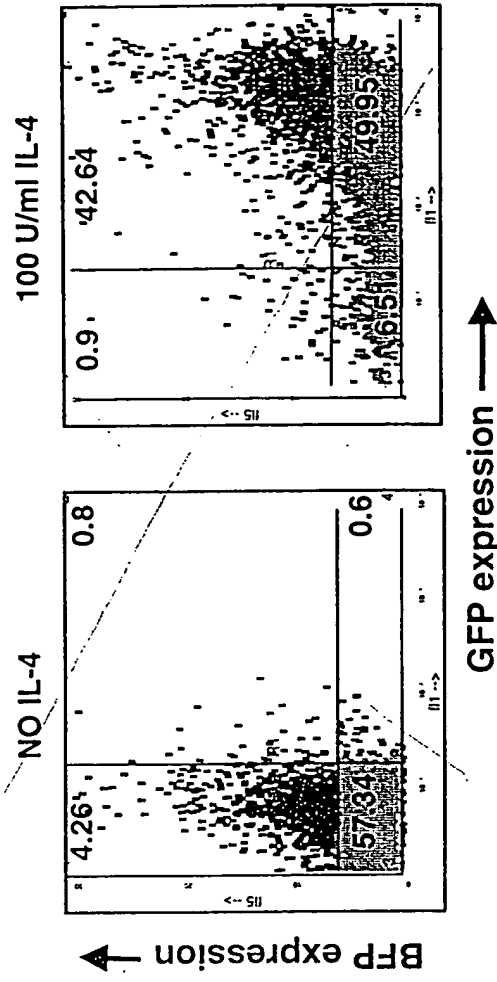
Reporter Line Infected with BFP Construct

Library construct



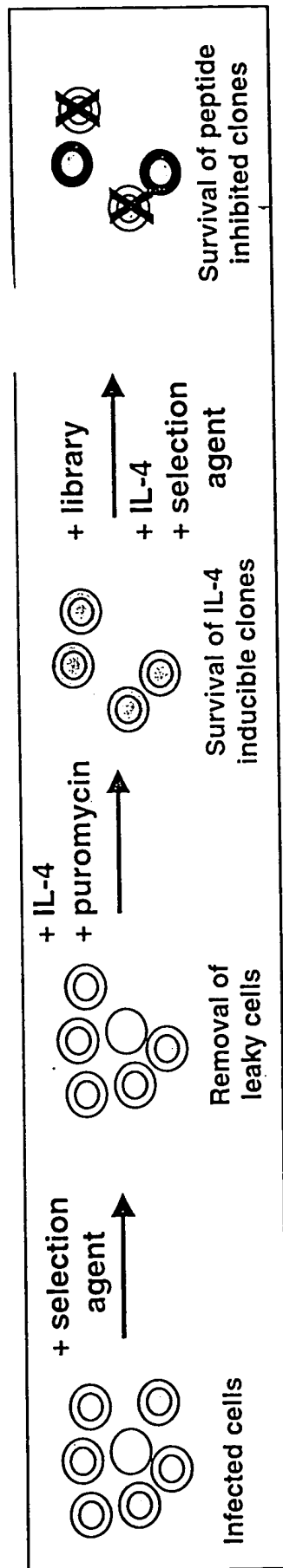
BFP, blue fluorescent protein

FACS profile of cells with both reporter and peptide library

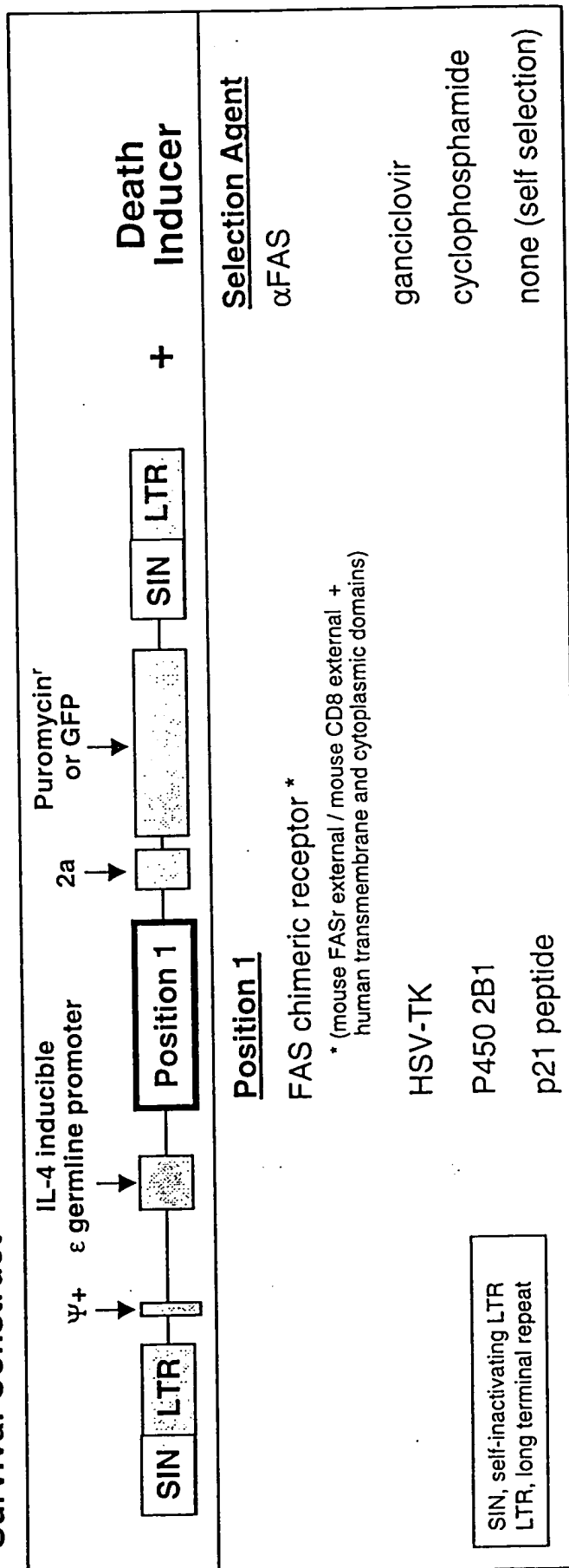


Appendix C

Screen for Peptide Inhibitors of the Germline ϵ Promoter



Survival Construct



Appendix D

All components are cassetted for flexibility

FIGURE 11A-1

1-845 CMV promoter/R/U5 5' LTR
 1322 GAG ATG-ATC mutation
 850-2100 extended ψ region
 2146-2173 two Bstx1 peptide cloning sites
 2205-2723 ECMV IRES (cloned as EcoR1/MscI fragment from
 pCITE-4a [Novagen])
 2746-3465 GFP coding region
 3522-4115 3' LTR
 4122-6210 pGEM backbone (pUC origin, ampR)

ATCACGAGGCCCTTTCGTCTTCAAGAACAGCTTTGCTCTTAGGAGTTTCCTAATACATCC
 CAAACTCAAATATATAAAGCATTGACTTGTTCTATGCCCTAGTTATTAATAGTAATCAA
 TTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAA
 ATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCCATGACGTCAATAATGACGTATG
 TTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
 AAAC TGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
 TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTC
 CTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGC
 AGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCA
 TTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAA
 GCAGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGGGCGCCAGTCCCTCCGATTGACT
 GAGTCGCCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGCAAGTTGCATCCGACTTGTGGT
 CTCGCTGTTCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTT
 CATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACCACCGACCCACCACCG
 GGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTGA
 TTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGG
 TGGAAGTACGAGTTTCGGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTCGG
 GGGCCGTTTTTGTGGCCCGACCTGAGTCCAAAAATCCCGATCGTTTTGGACTCTTTGGTG
 CACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCC
 CGCCTCCGTCTGAATTTTTGCTTTTCGGTTTGGGACCGAAGCCGCGCCGCGCTTGTCT
 GCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATA
 TCGGCCCCGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATG
 TCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCT
 GCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAG
 ACCTCATCACCCAGGTTAAGATCAAGGTCTTTTACCTGGCCCGCATGGACACCCAGACC
 AGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGC
 CCTTTGTACACCCTAAGCCTCCGCCTCCTCTTCCCTCCATCCGCCCCGTCTCTCCCCCTTG
 AACCTCCTCGTTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAG
 GCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCGCCCCCTTGTAACCTTCC
 CTGACCCTGACATGACAAGAGTTACTAACAGCCCCCTCTCTCCAAGCTCACTTACAGGCTC
 TCTACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAAGTGG
 ACCGACCGGTGGTACCTCACCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACC
 AGACTAAGAACCTAGAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCA
 CCGCCCTCAAAGTAGACGGCATCGCGCTTGGATACACGCCGCCACGTGAAGGCTGCCGA
 CCGCGGGGGTGGACCATCCTCTAGACTGCCGGATCTCGAGGGATCCACCACCATGGACCC
 CCATTAAATTGGAATTCCTGCAGCCCGGGGGATCCACTAGTTCTAGAGCGAATTAATTCC

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FIGURE 11A-2

GGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTG
TCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGT
TGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAG
CGACCCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGC
CACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGA
TAGTTGTGGAAGAGTCAAATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATG
CCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACAT
GTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCCGAACCACGGGGACGTGGTTTTCCT
TTGAAAAACACGATGATAATATGGGGGATCCACCGGTGCGCACCATGGTGAGCAAGGGCG
AGGAGCTGTTACCGGGGTGGTGCCCATCTGGTTCGAGCTGGACGGCGACGTAAACGGCC
ACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCCTGA
AGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGA
CCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCA
AGTCCGCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCA
ACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGC
TGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC
ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAC
TCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGA
ACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGT
CCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGA
CCGCCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCTCGACGA
TAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTA
GGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGA
GAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGGCAAACA
GGATATCTGTGGTAAGCAGTTCTTGCCCCGGCTCAGGGCCAAAGAACAGATGGAACAGCTG
AATATGGGGCAAACAGGATATCTGTGGTAAGCAGTTCTTGCCCCGGCTCAGGGCCAAAGAA
CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTC
CAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCG
CTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
TCACTCGGGGCGCCAGTCCCTCCGATTGACTGAGTCGCCCCGGGTACCCGTGTATCCAATAA
ACCCTCTTGACAGTTGCATCCGACTTGTGGTCTCGCTGTTTCCTTGGGAGGGTCTCCTCTGA
GTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTCGACTTGTGGTCTCGCTGCCTTGG
GAGGGTCTCCTCTGAGTGAATTGACTACCCGTCAGCGGGGGTCTTCACATGCAGCATGTAT
CAAAATTAATTTGGTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTTGCATTAAT
GAATCGGCCAACGCGCGGGGAGAGGCGGTTTGGCTATTGGCGCTCTTCCGCTTCTCTCGCT
CACTGACTCGCTGCGCTCGGTCTGCTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGC
GGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAGG
CCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCG
CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG
ACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCGAC
CCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGCGCTTTCTCA
TAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCAAGCTGGGCTGTGT
GCACGAACCCCCCGTTAGCCCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAGTC
CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC
TAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT
TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAA
GCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG
GTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAA
AAGGATCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTGCGCAAATCAATCTAAAG
TATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTC
AGCGATCTGTCTATTTCTGTTTATCCATAGTTGCCTGACTCCCCGTGCTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGG

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FIGURE 11A-3

TCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAG
TAGTTCGCCAGTTAATAGTTTTCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTC
ACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTAC
ATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAG
AAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTAC
TGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTG
AGAATAGTGATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGC
GCCACATAGCAGAACTTTAAAAAGTGCTCATCATTTGGAAAACGTTCTTCGGGGCGAAAACT
CTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTG
ATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAA
TGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTT
TCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATG
TATTTAGAAAAATAACAAATAGGGGTTCGCGCACATTTT

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FIGURE 11B-1

1-845 CMVpormoter/R/U5 5' LTR
 1322 GAG ATG-ATC mutation
 850-2100 extended □ region
 2151-2865 GFP coding region
 2866-2894 GGS SGG linker
 2895-2952 FMDV 2a cleavage sequence
 2953-3004 Bstx1/Bstx1/HinD3/Hpa1/Sal1/Not1 polylinker
 3052-3645 3' LTR
 3652-5715 pGEM backbone (pUC origin, ampR)

ATCACGAGGCCCTTTCGTCTTCAAGAACAGCTTTGCTCTTAGGAGTTTCTAATACATC
 CCAAACCTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGTTATTAATAGTAATC
 AATTACGGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGG
 TAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAATGACG
 TATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTT
 ACGGTAAACTGCCCACCTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTA
 TTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGG
 GACTTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCG
 GTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGGACTCACGGGGATTTCGAAGTC
 TCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCA
 AAATGTTCGTAACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGA
 GGTCTATATAAGCAGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGGGCGCCAGTC
 CTCCGATTGACTGAGTCGCCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGCAAGTTGCA
 TCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGT
 CAGCGGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACC
 ACCGACCCACCACCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTC
 TAGTGTCTATGACTGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGT
 ATCTGGCGGACCCGTGGTGGAAGTACGAGTTCGGAACACCCGGCCGCAACCCTGGGAG

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FIGURE 11B-2

ACGTCCCAGGGACTTCGGGGGCGGTTTTGTGGCCCGACCTGAGTCCAAAAATCCCGAT
CGTTTTGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGA
CGAGAACCTAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTTCGGTTTGGGACCGAA
GCCGCGCCGCGCGTCTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTG
TTTCTGTATTTGTCTGAAAATATCGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTT
GACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCA
AGAAGAGACGTTGGGTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCCGATGG
CCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTAAAGATCAAGGTCTTTTC
ACCTGGCCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTGG
CTTTTGACCCCCCTCCCTGGGTCAAGCCCTTGTACACCCTAAGCCTCCGCCTCCTCTT
CCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTTCGACCCCGCCTCGATCCTC
CCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTAT
ATGGGGCACCCCCGCCCCCTTGTAACCTTCCCTGACCCTGACATGACAAGAGTTACTAAC
AGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAG
ACCTCTGGCGGCAGCCTACCAAGAACAACCTGGACCGACCGGTGGTACCTCACCTTACC
GAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCTGG
AAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATCGC
AGCTTGGATACACGCCGCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTA
GACTGCCGGATCTCGAGGGATCCACCATGGTGAGCAAGGGCGAGGAGCTGTTACCGGG
GTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTG
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCA
CCGGCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAG
TGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCC
CGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCC
GCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATC
GACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCA
CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCC
GCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCC
ATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCT
GAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCG
CCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGAATTCGGAGGTGGCAGCGGTGGC
GGTCAGCTGTTGAATTTTGACCTTCTTAACTTGCGGGAGACGTGAGTCCAACCCTGG
GCCACCACCACCATGGAAGCTTCCATTAAATTGGTTAACGTGACGCGGCCGCTCGAC
GATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCT
GTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAAATACATAA
CTGAGAATAGAGAAGTTCAGATCAAGGTGAGGAACAGATGGAACAGCTGAATATGGGCC
AAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAA
CAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG
CCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA
GATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCA
ATCAGTTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGC
CCACAACCCCTCACTCGGGGCGCCAGTCCCTCCGATTGACTGAGTCGCCCCGGGTACCCGT
GTATCCAATAAACCCCTCTTGCAAGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAG
GGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTTCAATTTCCGACTTGTGGT
CTCGCTGCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTCA
CATGCAGCATGTATCAAAATTAATTTGGTTTTTTTTTCTTAAGTATTTACATTAAATGGC
CATAGTTGCATTAAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCCTATTGGCGCT

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FIG 12A

(1) C12ScFas Survival construct

C12ScFas: epsilon-cFas(CD95)-Ires-Hygro-BGH PolyA put into C12s vector backwards so that no leaky transcription happens through the cmv promoter.

atcacgaggccctttctgtcttcaagaacagcttttgcctcttaggagtttcttaatacatcccaaaactcaaatatataaagc
atttgactgttctctatgccctagttatttaataagtaatacaattacggggtcattagttcatagcccatatattggagttccg
cgttacataacttacggtaaatggcccgctgggtgacccgccaacgaccccgccattgacgtcaataatgacgtatg
tcccatagtaacgccaatagggaactttccattgacgtcaatgggtggagattttacggtaaactgcccacttggcagta
catcaagtgtatcatatgccaagtacgccccctattgacgtcaatgacggtaaatggcccgctggcattatggccagta
catgaccttatgggaactttctacttggcagtaacctctacgtattgactcatcgctattaccatgggtgatcggttttggc
agtacatcaatggcggtggatagcggtttgactcacggggatttccaagtctccaccccatgacgtcaatgggagtttg
tttgggacccaaaatcaacgggactttccaaaatgtcgtacaactccgccccattgacgtcaatggcggttaggcatgt
acggtgggaggtctatatagcagagctcaataaaagagcccaaacccctcactcggggcgccagctcctccgattgact
gagtcgcccgggtgataccggtgtatccaataaacctcttgcaggttagtcatcgacttgtggtctcgctgttcttgggagg
tctcctctgagtgattgactaccggtcagcggggtcttctatttgggggtcgctccgggatcgggagacccctgcccag
ggaccaccgacccaccacgggaggttaagctggccagcaacttatctgtgtctgtccgattgtctagtgtctatgactga
ttttatgcgctcgctcggtacttagtttagctaactagctctgtatctggcgacccgtggtggaactgacgagttcgga
caccggcgcaaacctgggagacgtcccagggacttcggggcggttttggggccgacctgagtcgcaaaaatcccgga
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CAGGGTGCAGTTTGTTCCTTCTAAACCATGCTCTTCATCGCAGAGTGTGCATCTTCTGCATTTATCAGCATAATGGT

TCTTGTCATGTACTCTTCCCTTCTGTGCATGGGGCACAGGTTGGTGTACCCCCATTCATTTTGCAGTCTCTCAACTTTT

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THE

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CCGGAAGCATAAAGTGTAAGCCTGGGGTGCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCGT
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TGCCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGCGCTTTTCTCATAGCTCACGCTGTAGGTATCTC
AGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCTTATCCGG
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TACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGGAGACCCACGCTCACCGGCTCCAGATTATCAGCA
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CCGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGTTTGGCGAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTAC
GCTCGTCTGTTTGGTATAGGCTTCATTCAGCTCCGGTCCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAA
AAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGTCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGC

FIG 12C

ACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGagtactcaaccaagtcattctgag
aatagtgtatgcggcgaccgagttgctcttgcccggcgtcaacacgggataataccgcgccacatagcagaactttaaaa
gtgctcatcattggaaaacgttcttcggggcgaaaactctcaaggatcttaccgctgttgagatccagttcgatgtaacc
cactcgtgcacccaactgatcttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaatg
ccgcaaaaaaggggaataagggcgacacggaaatggtgaatactcatactcttcctttttcaatattattgaagcatttat
caggggtattgtctcatgacattaacctataaaaaataggcgt

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FIG 13A

(2) Ahhhh: Survival construct

2.) Ahhhh: epsilon-cFas' (CD8 or mLy2)-Ires-Hygro-BGHpolyA also in C12s backwards

atcacgaggccctttctgtcttcaagaacagctttgtctttaggagtttcttaatacatccaaactcaaatatataaagc
atttgacttgttctatgccctagttatttaadtagtaataacacggggtcattagttcatagcccatatatggagttccg
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TGCTATTGTCTTCCCAATCTTCCCCCTTGCTGTCTTCCCCACCCACCCCAAGGATAGAATGACACCTACTCAGACAA

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GTAGTTCCGCAAGTAAAGTTTGGCGAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTTGGTATG

FOI b7E b7C b7D

FIG 13C

GCTTCATT CAGCTCCGGT TCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTT
CGGTCTCTCCGATCGTTGTCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTA
CTGFCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGagtgactcaaccaagtcattctgagaatagtgtatgcggcgca

1 cccgagttgctcttgcgccggcgtcaacacgggataataaccgcgccacatagcagaactttaaaagtgtcatcattggaaa
 2 acgttcttcggggcgaaaactctcaagatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaact
 3 gatcttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaatgccgcaaaaaagggaata
 4 agggcgacacggaaatgttgaatactcatactcttctctttttcaatattattgaagcatttatcagggttattgtctcat
 5 gacattaacctataaaaaataggcgt